

```

1 gcgtctccac ccctcagcgg gcggcggtga gtgcgccagg ccagcgccgg cgtgggaccg
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121 gagtttagtg acccttccaa AATGGCTGCT ATTAAGGAAG AGAGACAGGT GGAAGATTAC
181 AAGAGAAAAA GGAAGACGAT CAGCACAGGC CATGAGCCTA AGGAGCCAGA GCAGTTGAGA
241 AAGCTGTTCA TTGGAGGTCT GAGCTTCGAG ACGACGGATG ATAGCTTGAG AGAGCACITT
301 GAAAAATGGG GCACACTCAC GGACTGTGTG GTGATGAGAG ACCCACAAAC AAAACGTTCC
361 AGAGGCTTTG GCTTTGTTAC TTACTCTTGC GTGGAAGAGG TGGATGCGGC CATGAGCGCT
421 CGACCACATA AGGTGGATGG ACGTGTGGTT GAACCAAAGA GAGCAGTTTC AAGGGAGGAT
481 TCTGTAAAGC CTGGGGCGCA TCTCACAGTA AAGAAAATAT TTGTTGGTGG CATTAAAGAA
541 GATACAGAAG AATATAATTT AAGGGGGTAC TTTGAAACAT ATGGCAAGAT CGAAACGATA
601 GAAGTCATGG AAGACAGACA AAGTGGAAAG AAAAGAGGCT TCGCTTTTGT AACTTTTGAT
661 GATCACGATA CAGTTGATAA AATTGTTGTT CAGAAATACC ATACTATAAA TGGTCATAAC
721 TCGGAAGATA AAAAAGCACT CTCAAAACAA GAGATGCAGA CTGCCAGCTC TCAGAGAGGT
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961 TATGGAGGTG GTCCTGGCTA TGGCAGCAGA GGGGGTTATG GTGGTGGTGG AGGACCAGGA
1021 TATGGAAACC CAGGTGGTGG ATATGGAGGT GGAGGAGGAG GATATGGTGG CTACAATGAA
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1141 TACAGTGGAC AGCAGCAGTC CAATTACGGT CCCATGAAAG GTGGTGGCAG TTTTGGTGGT
1201 AGAAGTTCAG GCAGTCCCTA TGGTGGTGGT TATGGATCTG GAAGTGGAAAG TGGGGGCTAT
1261 GGTGGTAGAA GATTCTaaaa atgctaccag aaaaagggt acagtcttta gcaggagaga
1321 gagcgaggag ttgtcaggaa agctgcaggt tactttgaga cagtcgtccc aaatgcatta
1381 gaggaactgt aaaaatctgcc acagaaggaa cgatgatcca tagtcagaaa agttactgca
1441 gcttaaacag gaaacccttc ttgttcagga ctgtcatagc cacagtttgc aaaaagagca
1501 gctatttggt aatgcaatgt agtgtcggtta gatgtacatc ctgaggtctt tatctgttgt
1561 agctttgtct ttcttttttc tttttatttt cccattacat caggtatatt gccctgtaaa
1621 ttgtgtagt ggtaccagga ataaacaaat taaggaatth ttggcttttc aaaaaaaa
1681 aaaaaaaa

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Fig. 1a

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CHKA1 - MAAIKEEREVEDYKRRKTIISTGHEPKPEQLRKLFIGGLSFETDDSLR -50
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
HUMA1 - M-----SKSESPKEPEQLRKLFIGGLSFETTTDESLR -31

CHKA1 - EQFEKWGTLTDCVVRDPQTKRSRGFGFVTYSCVEEVDAAAMNARPHKVDG -100
      || | | | | | | | | | | | | | | | | | | | | | | | | | |
HUMA1 - SHFEQWGTLDVVRDPNTKRSRGFGFVTYATVEEVDAAAMNARPHKVDG -81

CHKA1 - RVVEPKRAVSREDSVKPGAHLTVKKIFVGGIKEDTEEYNLRGYFETYGKI -150
      | | | | | | | | | | | | | | | | | | | | | | | | | |
HUMA1 - RVVEPKRAVSREDSQRPGAHLTVKKIFVGGIKEDTEEHLRDYFEQYGKI -131

CHKA1 - ETIEVMEDRSGKKRGFAFVTDDHDTVVDKIVVQKYHTINGHNCEDEKAL -200
      | | | | | | | | | | | | | | | | | | | | | | | | | |
HUMA1 - EVIEIMTDRSGKKRGFAFVTDDHDSVDKIVIQKYHTVNGHNCEVRKAL -181

CHKA1 - SKQEMQTASS-QRGRGGSGNFMGRGNFGGGG-----NFGRGGNFGG -242
      | | | | | | | | | | | | | | | | | | | | | | | | | |
HUMA1 - SKQEMASASSSQGRSGS-----GNFGGGGGGGFGGNDNFGRGNFSG -224

CHKA1 - RGGYGGGGGGGSGSFGGGDGYNGFGDGGNYGGGPGYGSRGYGGGGGP -292
      | | | | | | | | | | | | | | | | | | | | | | | | | |
HUMA1 - RGGFGGSRGGGGYGGG---GDGYNGFGNDGS----- -252

CHKA1 - GYGNPGGGYGGGGYGGYNEGGNFGGGNYGGSGNYNDFGNYSQQQSNY -342
      | | | | | | | | | | | | | | | | | | | | | | | | | |
HUMA1 - -----NFGGGGSYNDFGNYNQNS-SNF -273

CHKA1 - GPMKGGGSGGRRSSGSPYGGG-----YSGSGSGGGYG-GRRF -378
      | | | | | | | | | | | | | | | | | | | | | | | | | |
HUMA1 - GPMKGG-NFGGRRSSG-PYGGGGQYFAKPRNQGGYGGSSSSSYSGSGRRF -320

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Fig. 1b

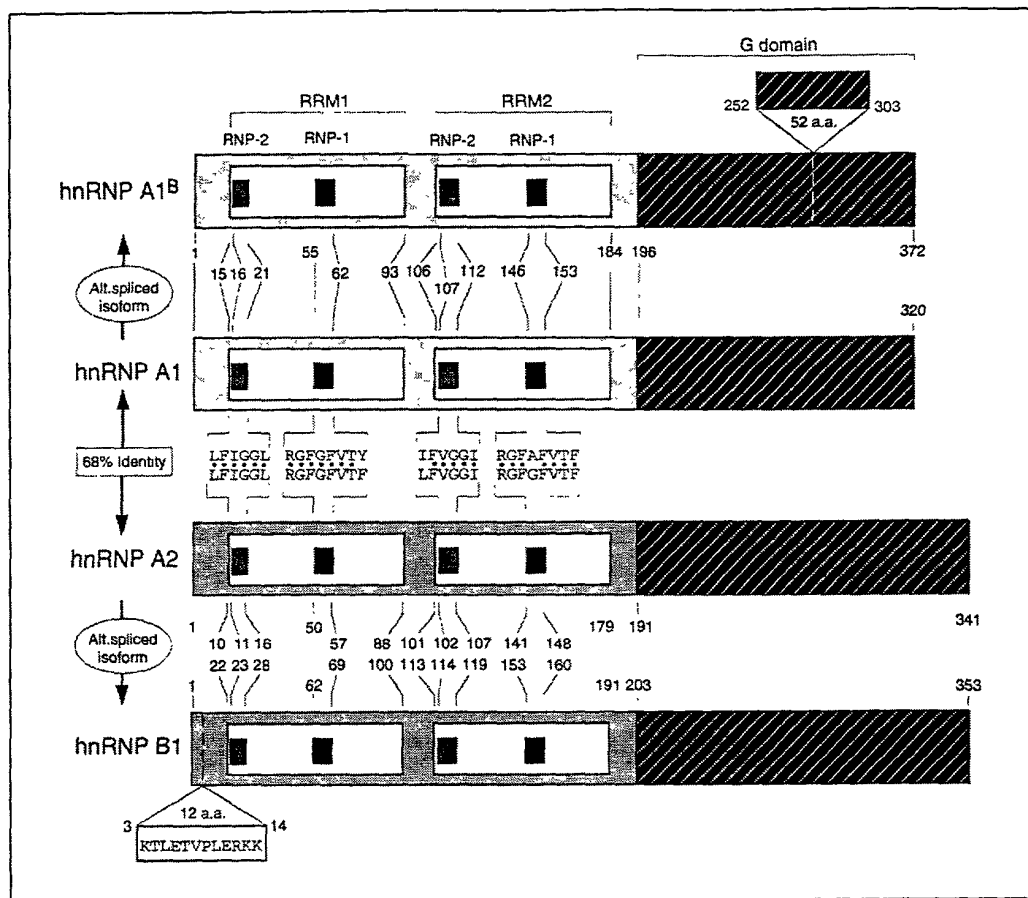


Fig. 2

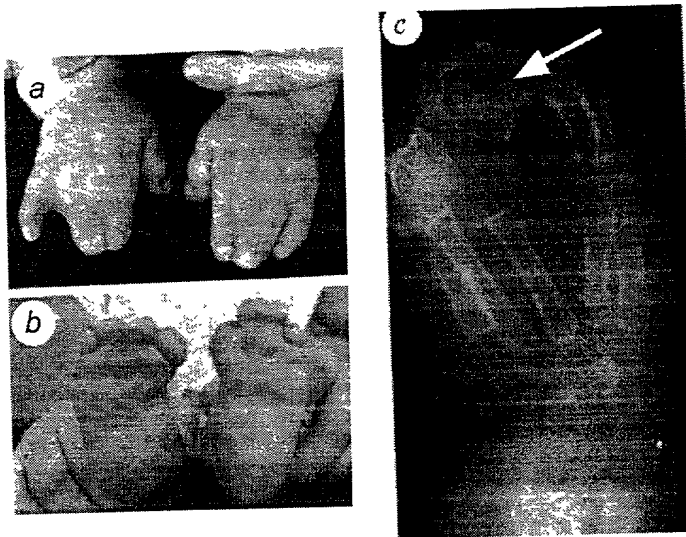


Fig. 3

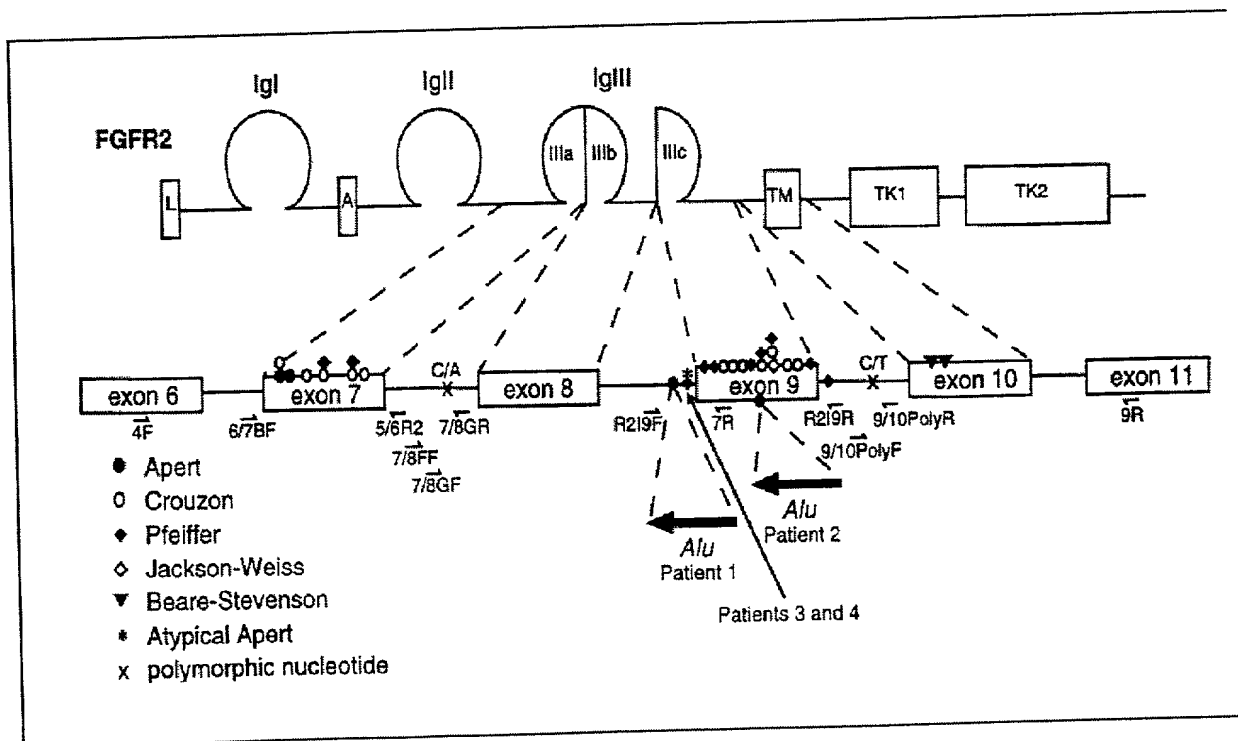
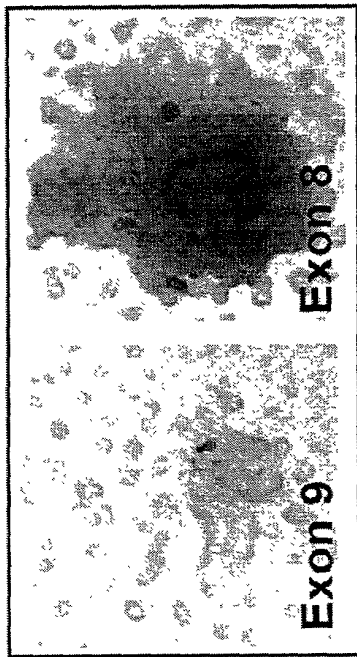
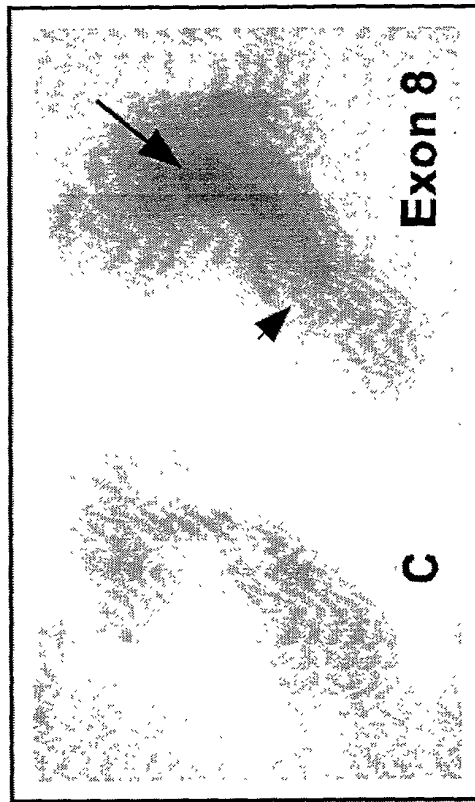


Fig. 4

A.



B.



C.

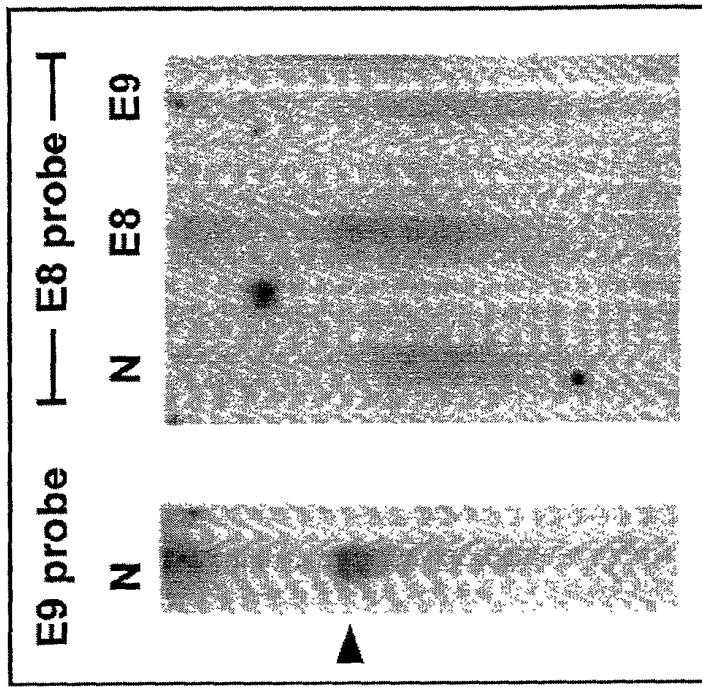


Fig. 5